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Query: 1 MATPRGLGALLLLLLLPTSGQEKTEPTEGPRNTC - LGSNNMYDIFNLNDKALCFCTKCRQS 58
MAT R LG L LLL + + E TE PRN C - L + YD F+LND A CPTKC QS
Sbjct: 17 MATARSLGLLFFLLF---TDSEETTEFLPRNVCRRILQEGHYDTFDLNDTAQCFCTKCGQS 187

Query: 59 SDSCNVENLQRYWLNIEAHLMEKGLTKQVNTPFLKALVQNLSNTAEDFYFSLEPSQVPR 118
C+V NLQRYWLNIE++L++ + + V+ PF+KAL+QN+ST+ +ED +SL SQ+PR
Sbjct: 188 HSPCDVGNLQRYWLNIESYLLNSM-ETVDMPFVKALIQNISTDVSDDLYSMLMSQIPR 364

Query: 119 QVMKDEDKPPDRVRLPKSLFRSLPGNRSSVRLAVTLIDIGPTGLFKGPRLGDLGDSGVLN 178
QVM+ ED+P + VRLP+L+L+LPGNRS VRLA+T+LDIG G +FKG+P+ QS VLN
Sbjct: 365 QVMQGEDEPADGVRLPKSLFGALPGNRSVRLAITVLDIGAGNVFKGPKLLEDKGSSVLN 544

Query: 179 NRLVGLSVGQMHHVTKLAEPLEIVFSHQRPPPNMTL 213
NRMVGLSVGQM T L+EP+EI FSH+R P P M L
Sbjct: 545 NRMVGLSVGQMHAATGLSEPVETTFSHERPAPMIL 649

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Score = 84.7 bits (206), Expect(3) = 0.0
Identities = 41/54 (75%), Positives = 45/54 (82%), Gaps = 1/54 (1%)
Frame = +3

Query: 497 PLGLSTVYIFALFNSLQGVFICCWFTILYLPSQSTTVSSS-TARLDQAHSASQE 549
P GLST+Y+F L NSLQG+FI CWF ILY P+QSTT SSS TARLDQAHS SQE
Sbjct: 1599 PPGLSTIYVFTLLNSLQGLFIFCWFIIILYFPTQSTTASSSGTARLDQAHSVSQE 1760